

A

MUSCLE-N
m MGGQITRNTIHD-----SIGGSFPVPS-----HRCHHKQKHCPPTLSG----

BRAIN-N
m MGNNFSSVSSLQRGNPSRASRG---HPQNLKE-----SIGGSFPVPS-----HRCHHKQKHCPPTLSG---- 55
r MGNNFSSVSSLQRGNPSRASRG---HPQNLKD-----SIGGSFPVPS-----HRCHHKQKHCPPTLSG---- 55
h MGNNFSSVSSLQRGNPSRASRG---HPQNLKD-----SIGGSFPVPS-----HRCHHKQKHCPPTLSG---- 55
d MGLSDIPANYMQGSHPHLTLHPQQQHQNQQHLQHLQMQQLHNAMPTPAQQAQVLAESNELLNMTKDKLSSKKKMLLKKIKKH FGL 90

NLS1
m -----GGLPATPLLFPHPTKSGQILMDLSHKAVKROASFCNAITFSNRPLIYEQVRLKITKQCCGSGAIGLGFSTKDPDSRIHPD 136
r -----GGLPATPLLFPHPTKSGQILMDLSHKAVKROASFCNAITFSNRPLIYEQVRLKITKQCCGSGAIGLGFSTKDPDSRIHPD 136
h -----GGLPATPLLFPHPTKSGQILMDLSHKAVKROASFCNAITFSNRPLIYEQVRLKITKQCCGSGAIGLGFSTKDPDSRIHPD 136
d VRRSPSSCPGPNNLFPLOFH-SVHCNIRISRDGTLARRFESFCRAITFSARPYRINERICVKFAEISNNNGGIRFGFTSNDP-VTLEG 178

NLS2
m -----GGLPATPLLFPHPTKSGQILMDLSHKAVKROASFCNAITFSNRPLIYEQVRLKITKQCCGSGAIGLGFSTKDPDSRIHPD 136
r -----GGLPATPLLFPHPTKSGQILMDLSHKAVKROASFCNAITFSNRPLIYEQVRLKITKQCCGSGAIGLGFSTKDPDSRIHPD 136
h -----GGLPATPLLFPHPTKSGQILMDLSHKAVKROASFCNAITFSNRPLIYEQVRLKITKQCCGSGAIGLGFSTKDPDSRIHPD 136
d VRRSPSSCPGPNNLFPLOFH-SVHCNIRISRDGTLARRFESFCRAITFSARPYRINERICVKFAEISNNNGGIRFGFTSNDP-VTLEG 178

NHR1
m SLPKYACPDIVSQSGFWAKALPEEFANECNIIAFWVDKKGVFYRINESAAMLFFSGVRRVDPGLWALVDVYGLTRVQLLDS----- 218
r SLPKYACPDIVSQSGFWAKALPEEFANECNIIAFWVDKKGVFYRINESAAMLFFSGVRRVDPGLWALVDVYGLTRVQLLDS----- 218
h SLPKYACPDIVSQSGFWAKALPEEFANECNIIAFWVDKKGVFYRINESAAMLFFSGVRRVDPGLWALVDVYGLTRVQLLDS----- 218
d TLPKYACPDITNRPGFWAKALPEEFANECNIIAFWVDKKGVFYRINESAAMLFFSGVRRVDPGLWALVDVYGLTRVQLLDS----- 218

LRS1 *
m SLPKYACPDIVSQSGFWAKALPEEFANECNIIAFWVDKKGVFYRINESAAMLFFSGVRRVDPGLWALVDVYGLTRVQLLDS----- 218
r SLPKYACPDIVSQSGFWAKALPEEFANECNIIAFWVDKKGVFYRINESAAMLFFSGVRRVDPGLWALVDVYGLTRVQLLDS----- 218
h SLPKYACPDIVSQSGFWAKALPEEFANECNIIAFWVDKKGVFYRINESAAMLFFSGVRRVDPGLWALVDVYGLTRVQLLDS----- 218
d TLPKYACPDITNRPGFWAKALPEEFANECNIIAFWVDKKGVFYRINESAAMLFFSGVRRVDPGLWALVDVYGLTRVQLLDS----- 218

O **PKB**
m ELVLBDCLRRSFTALRRSLRCEADE-----ARLSVSLCDLNVPGADGDDGAPPAG--CPIPNLSLNSQHSRALP-A 288
r ELVLBDCLRRSFTALRRSLRCEADE-----ARLSVSLCDLNVPGADGDDGAPPAG--CPIPNLSLNSQHSRALP-A 288
h ELVLBDCLRRSFTALRRSLRCEADE-----ARLSVSLCDLNVPGADGDDGAPPAG--CPIPNLSLNSQHSRALP-A 288
d PAALMATVBAQQQMPOAANASSALNSHHPHQSSRRSLPGHTAIEHLEERHVMPSLQSLHLAAGNGGVSASVEAAIAHDLANCLPPL 358

NHR2
m QLDG-----DLRFHALRAGAHVRILDEQIVARLEHGRDERALVFTSRPVSAETIFIKVTRSGGGRAALSFQVTTCDPGTLRFPADLFFS 373
r QLDG-----DLRFHALRAGAHVRILDEQIVARLEHGRDERALVFTSRPVSAETIFIKVTRSGGGRAALSFQVTTCDPGTLRFPADLFFS 373
h QLDG-----DLRFHALRAGAHVRILDEQIVARLEHGRDERALVFTSRPVSAETIFIKVTRSGGGRAALSFQVTTCDPGTLRFPADLFFS 373
d RYNANGRLIPVFFHNT-KERNVRLSQDRFVASRTESDFCQGYVFTARPIRIGEKLVQVLKTEQMYVGCALALGLISQNPAMLCQNDLIND 447

LRS2 *
m PEALVDRKEFWAVCR-VPGPLHSGDILGLVNNADGELHLSHNGAAGMQLCVDAQPLWMLFSLHCAITQVRIIGSTIMTERGGP----- 457
r PEALVDRKEFWAVCR-VPGPLHSGDILGLVNNADGELHLSHNGAAGMQLCVDAQPLWMLFSLHCAITQVRIIGSTIMTERGGP----- 457
h PEALVDRKEFWAVCR-VPGPLHSGDILGLVNNADGELHLSHNGAAGMQLCVDAQPLWMLFSLHCAITQVRIIGSTIMTERGGP----- 457
d SDFLDRPFWVWVSKDIAAAPQRGDEIAFVAPNGEVSISKNNGPAVVVMHVDQLCLWAFLDVYGSTQSLRMFRQQLPNMVAYPSQPQV 537

SP1
m ----SLPCSPASTPSPSALGIRLSD-----PILSTCGSGPLGGSAGG-----TAPNSPVSLPESFVTPGLGQWSD--- 519
r ----SLPCSPASTPSPSALGIRLSD-----PILSTCGSGPLGGSAGG-----TAPNSPVSLPESFVTPGLGQWSD--- 519
h ----SLPCSPASTPSPSALGIRLSD-----PILSTCGSGPLGGSAGG-----TAPNSPVSLPESFVTPGLGQWSD--- 519
d NVNASSSSACNAASSTRMLPMTESSSLNAGATAKLLHPSQLSVAQSTSTLASAGGVNGSRMISMPSNGDILQIQNGGGCTVLVVNLPP 627

O **SP2**
m ----SLPCSPASTPSPSALGIRLSD-----PILSTCGSGPLGGSAGG-----TAPNSPVSLPESFVTPGLGQWSD--- 519
r ----SLPCSPASTPSPSALGIRLSD-----PILSTCGSGPLGGSAGG-----TAPNSPVSLPESFVTPGLGQWSD--- 519
h ----SLPCSPASTPSPSALGIRLSD-----PILSTCGSGPLGGSAGG-----TAPNSPVSLPESFVTPGLGQWSD--- 519
d NVNASSSSACNAASSTRMLPMTESSSLNAGATAKLLHPSQLSVAQSTSTLASAGGVNGSRMISMPSNGDILQIQNGGGCTVLVVNLPP 627

RZD
m HMCLCYSCGLRLKKALH-ACCPICRRPKIKDIKTYRSS 574
r HMCLCYSCGLRLKKALH-ACCPICRRPKIKDIKTYRSS 574
h HMCLCYSCGLRLKKALH-ACCPICRRPKIKDIKTYRSS 574
d HMCMCYDCATEQWRGVGGGQCLCAVIRDVIRTYTT- 754

B

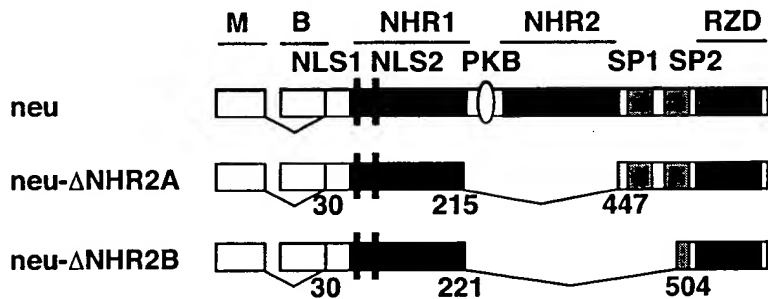
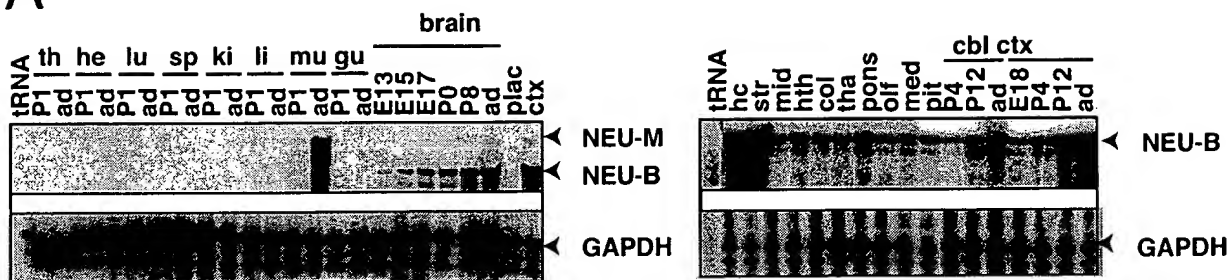


FIGURE 1

A



B

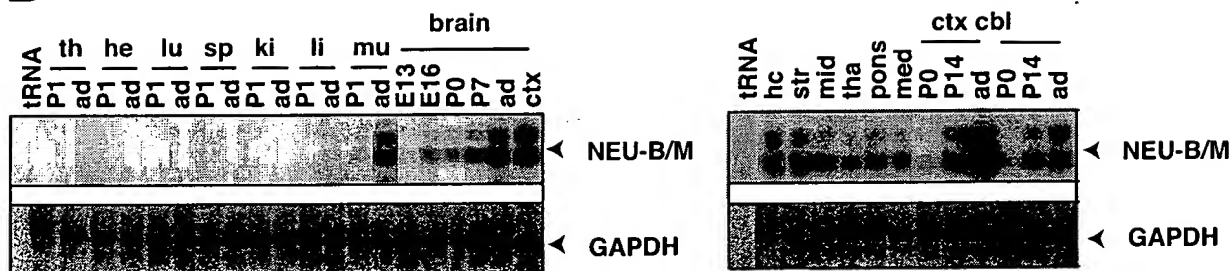


FIGURE 2

FIGURE 3

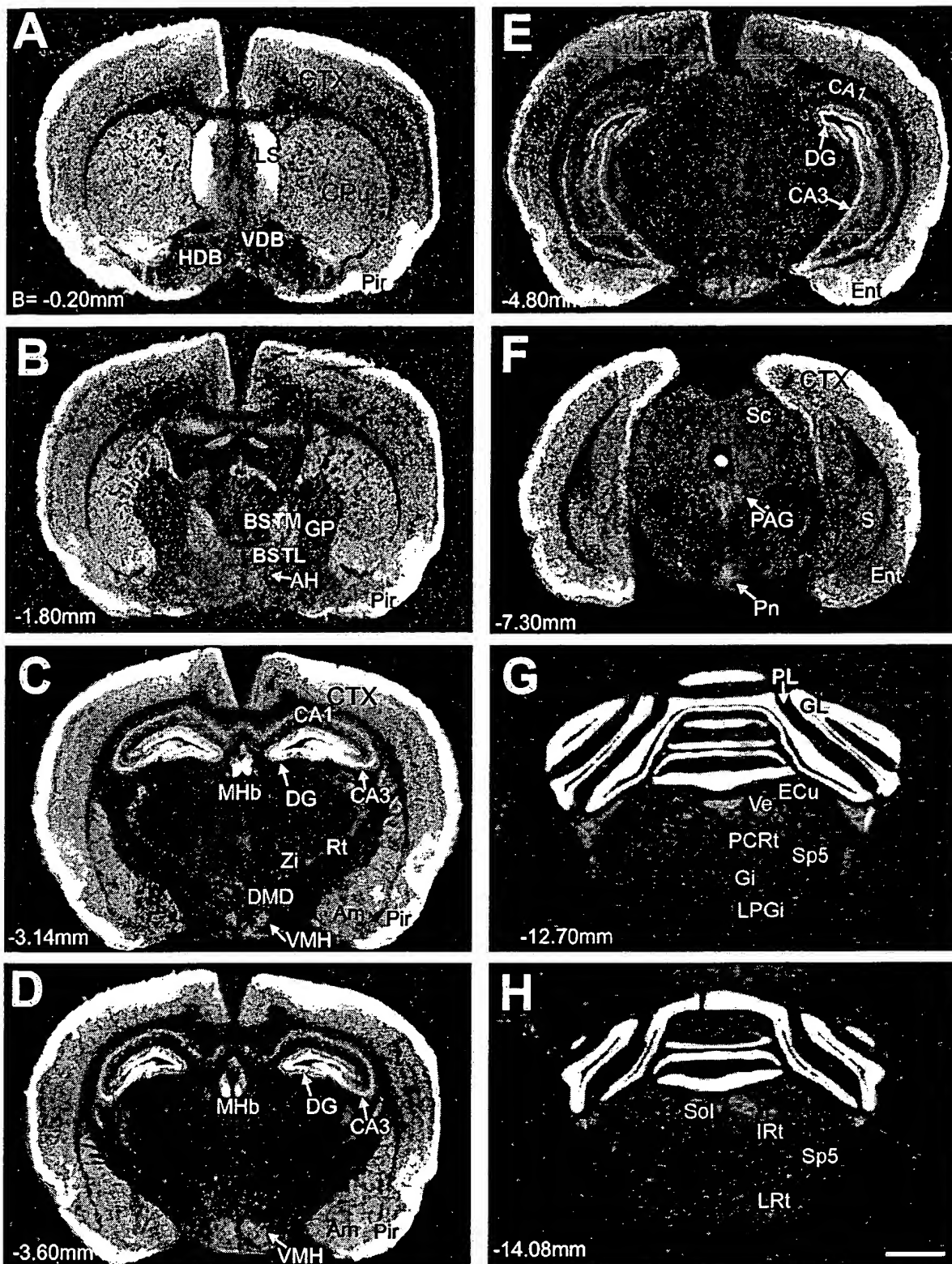


FIGURE 4

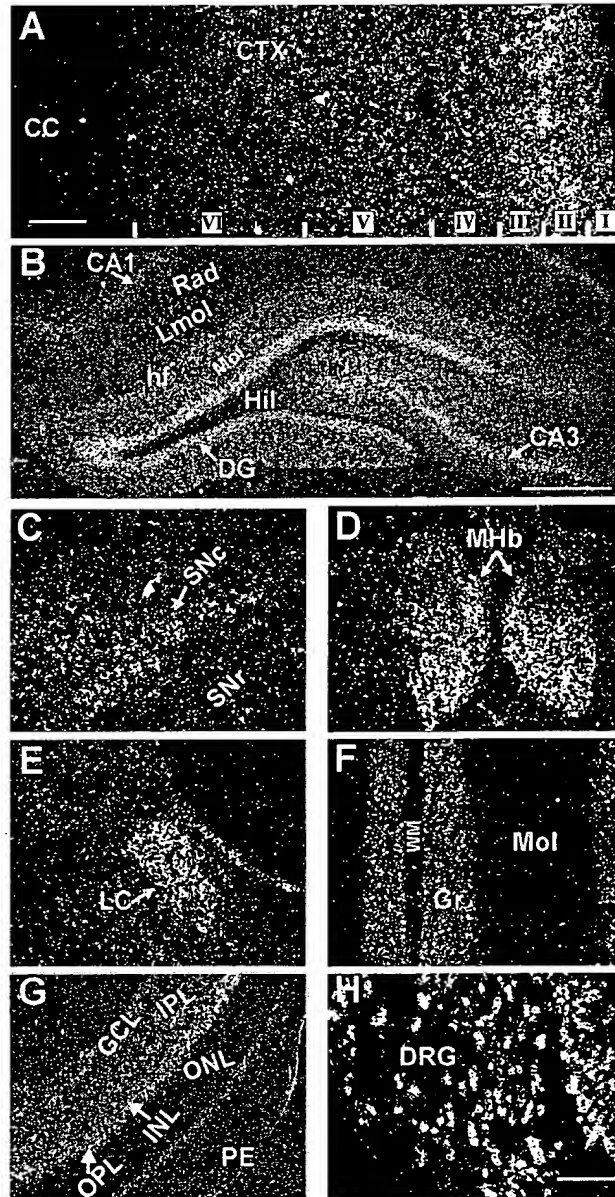


FIGURE 5

Figure 1 consists of 12 micrographs (A-L) arranged in a 4x3 grid, showing the distribution of ^{125}I -3 β -MBOA in various brain regions. The regions are labeled as follows:

- A:** CTX (Cerebral Cortex)
- B:** Hil (Hippocampal Interneuron Layer), DG (Dentate Gyrus), Mol (Molecular Layer)
- C:** Rad (Radiatum), CA3 (Cornu Ammonis 3), Or (Olfactory Bulb)
- D:** PoDG (Postdentate Gyrus), with two arrows pointing to specific features.
- E:** LS (Lateral Septum)
- F:** SNc (Substantia Nigra, pars compacta), with an arrow pointing to a specific feature.
- G:** GP (Globus Pallidus)
- H:** Sc (Septal Cortex)
- I:** Sc (Septal Cortex)
- J:** DRG (Dorsal Root Ganglion)
- K:** GL (Glia Limitans)
- L:** Pi (Pituitary Gland)

Each micrograph shows a different brain region with varying degrees of autoradiographic labeling. Arrows in panels D and F indicate specific features of interest. Scale bars are present in the bottom right of each panel.

FIGURE 6

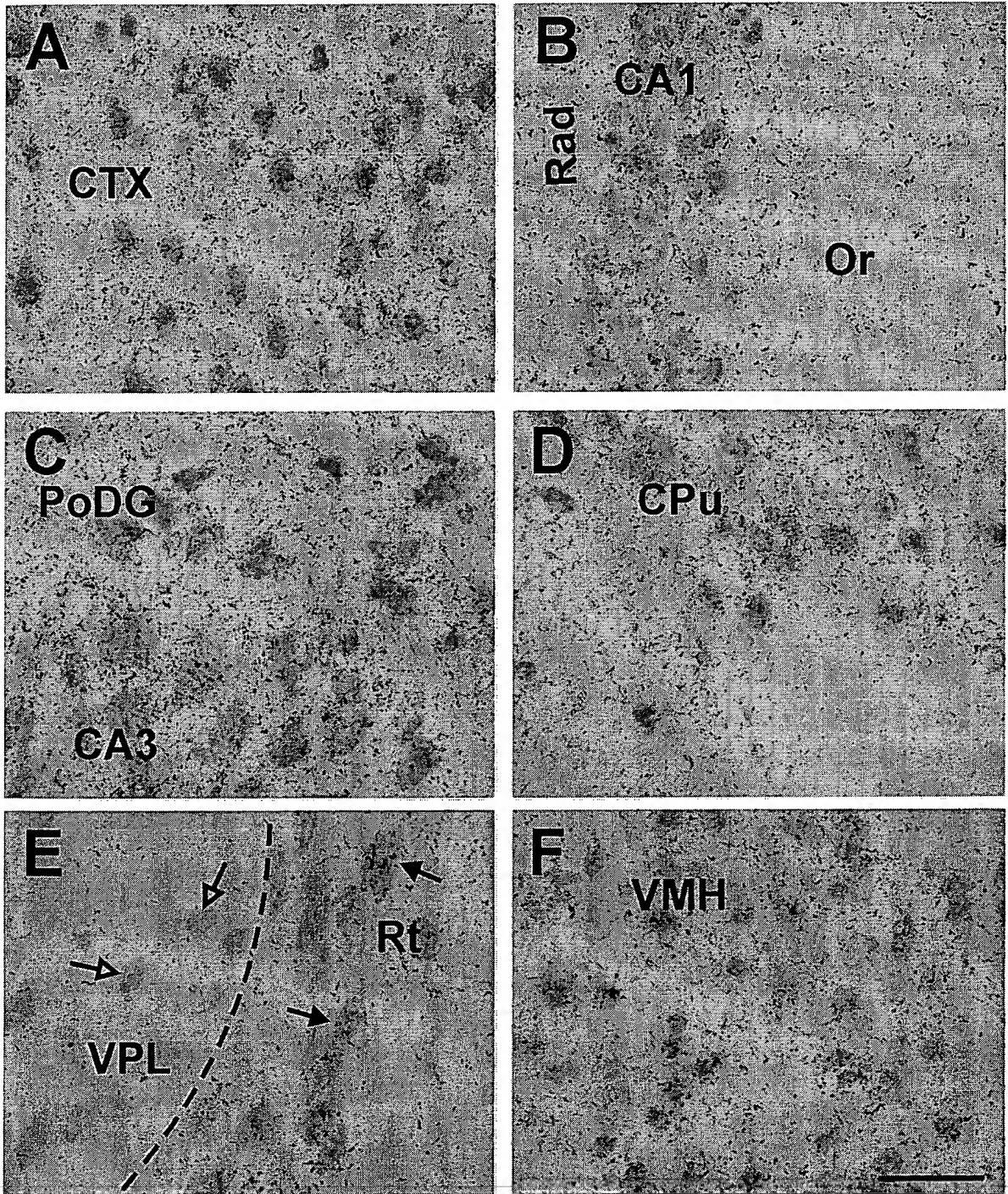


FIGURE 7

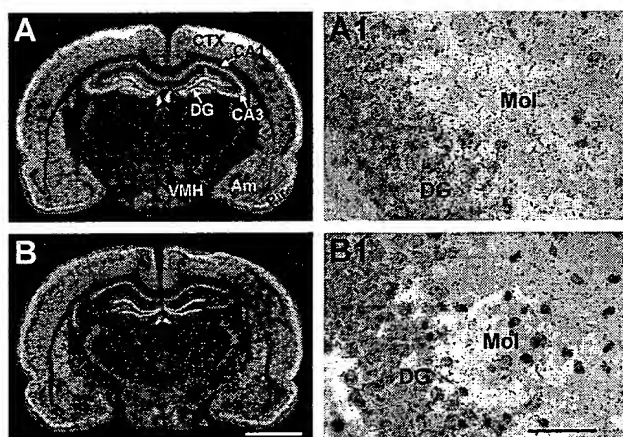


FIGURE 8

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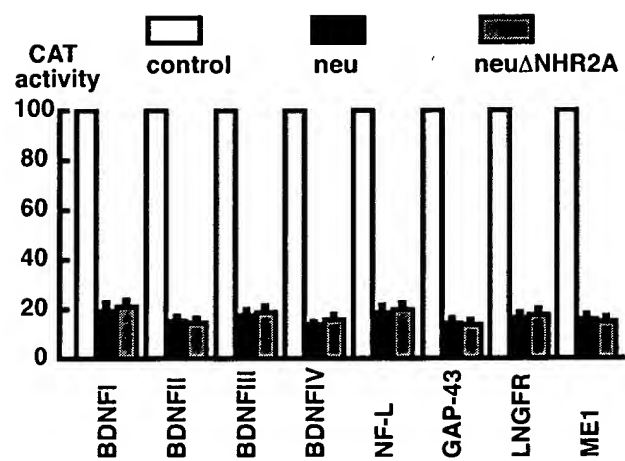


FIGURE 9

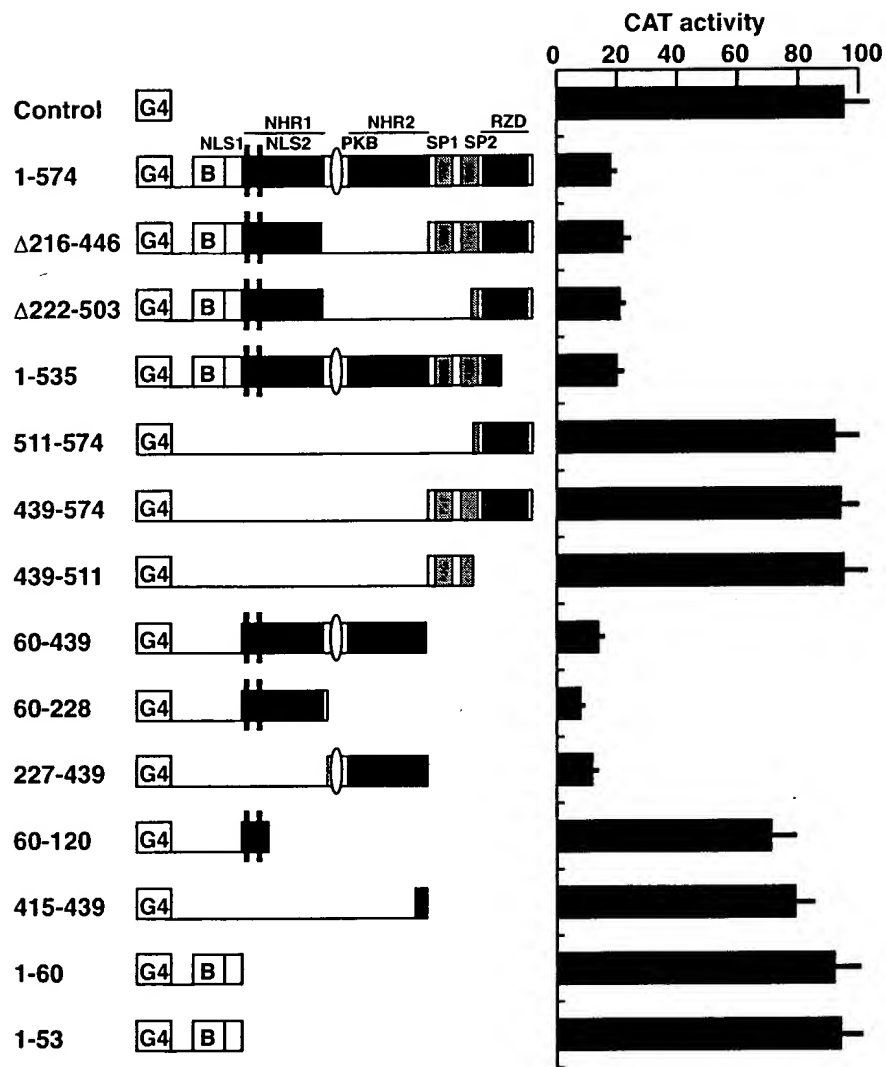


FIGURE 10

Figure 1 consists of eight panels (A-H) showing fluorescence microscopy images of cells expressing various GFP constructs. Panels A-F show cells expressing GFP-1-574, GFP-1-120, GFP-60-120, GFP-1-60, GFP-1-574 + LMB, and GFP-1-574 + RA, respectively. Panels G and H show cells expressing FLAG and EGFP, respectively. The images show the localization of the GFP constructs in the cytoplasm and nucleus.

FIGURE 11

h1I	FHPHTKGSQILMDLSHKAVKR-QASFCNAITFSNRPVLIYEQVRLKITTKKQCCWSGAILRL
h2I	FHAQAKGKNVRLDGHSRRATR-RNSFCNGVTETORPIRLYEQVRLRLVAVRPGWSGALRF
h3	FHAEAKGAQVRLDTRGCTAHR-RTTFHDGIVFSQRPVRLGERVALRVLREESGWCGGLRV
dI	FHS-VHGDNIRISRDGTLARR-FESFCRAITFSARPVRINERICVKFAEISNNWNGGIRF
dII	FHNTK-GRNVRLSQDRFVASRTESEDFCQGYVETARPIRIGEKLIVQVLKTEQMYVGALAL
h2II	FHATR-GPDVSLSADRKVAACAPRPDGGRTLVESERPRLRPGESLFVEVGRPGLAAPGALAF
h1II	FHALRAGAHRILDEQTVARVEHGRDERALVETSRPVRVAETIFVKVTRSGGAREGALS
h1I	GETSKDPSRIHPDSLPHYACPDLVSGSGFWAKAL-PEEFANEENITAFWVDKKGRVFHRI
h2I	GETAHDPSSLMSAQDIPKYACPDLVTRPGYFAKAL-PENLALRDTVLAYWADRHRGRVFYSV
h3	GETRLDPACVSVPSLPPFLCPDLEEQSPTWAAVL-PEGCALTGDVRFWVDRRGCLFAKV
dI	GETSNDEPVTLEG-TLPKYACPDLTNRPGFWAKAL-HEQYCEKDNILYYYVNGAGDVIIYGI
dII	GETSCNPAMLQP-NDLPNDSDFLLDRPEYVWVSKDIAAAPQRGDEIAFFVAPNGEVSISK
h2II	GETSCDPGVLRP-NELPADPDALLDRKEYWVVAR-AGPVPSGGDALSFTLRPGGDVLLGI
h1II	GVTTCDPGLRTP-ADLPFSPEALVDRKEFWAVCR-VPGPLHSGDILGLVVNADGELHLSH
h1I	NDSAVMLFFSGVVRTADPLWALVDVYG-LTRGVQLL
h2I	NDGEPVLFHCGVAVGGPLWALIDVYG-ITDEVQLL
h3	NAGCRLLREGVPVGAPLWAVMDVYG-TTKATELL
dI	NNEEKGVILTGIDTRSLLWTVIDIYG-NCTGIEFL
dII	NNGPAVVVMH-VDQSLQLWAFIDVYG-STQSLRMF
h2II	NGRPRGRLLC-VDTTQALWAFEAVRGGVAGQLRLL
h1II	NGAAAGMQLC-VDASQPLWMLGLHG-TITQIRIL

FIGURE 12

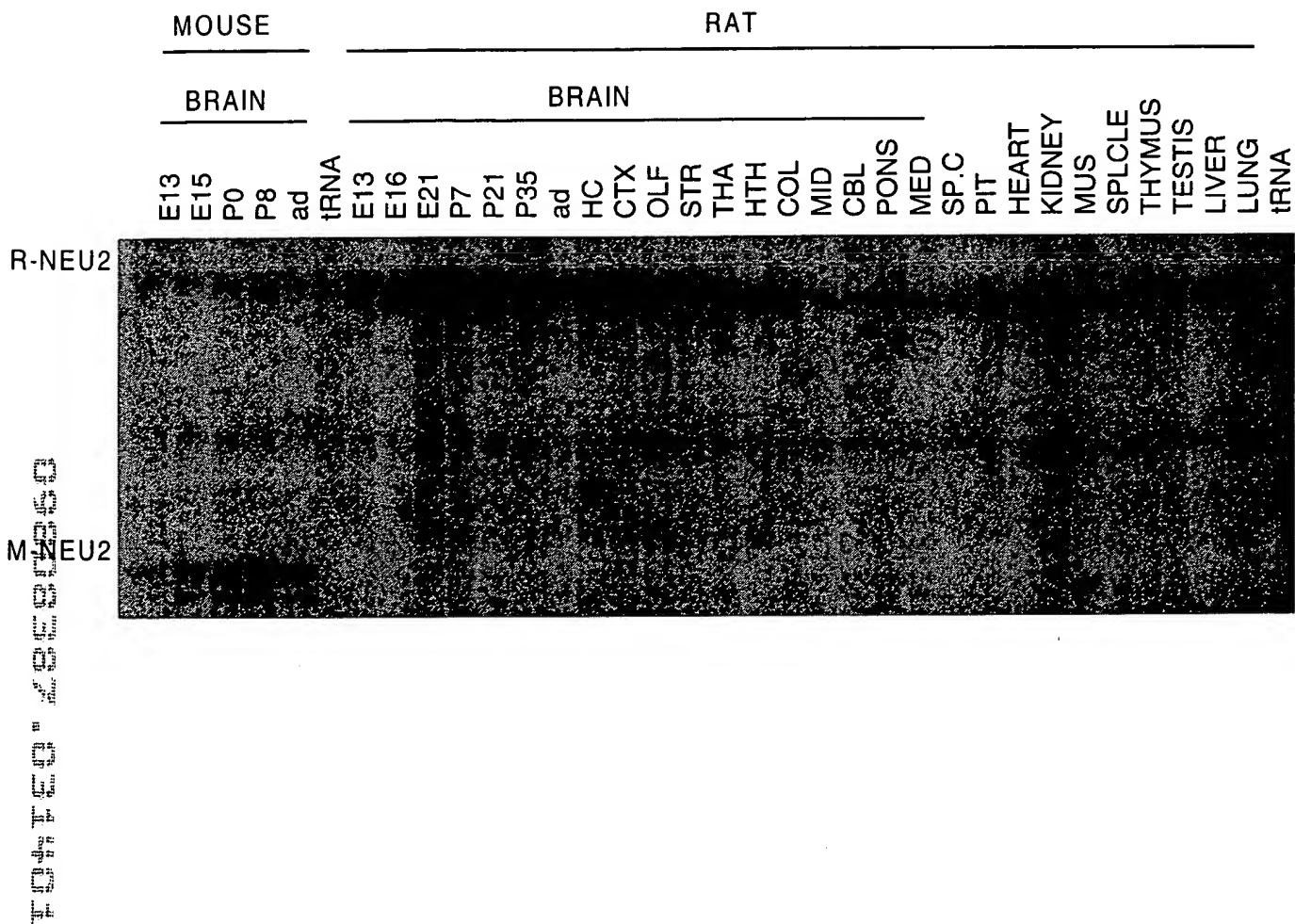


FIGURE 13

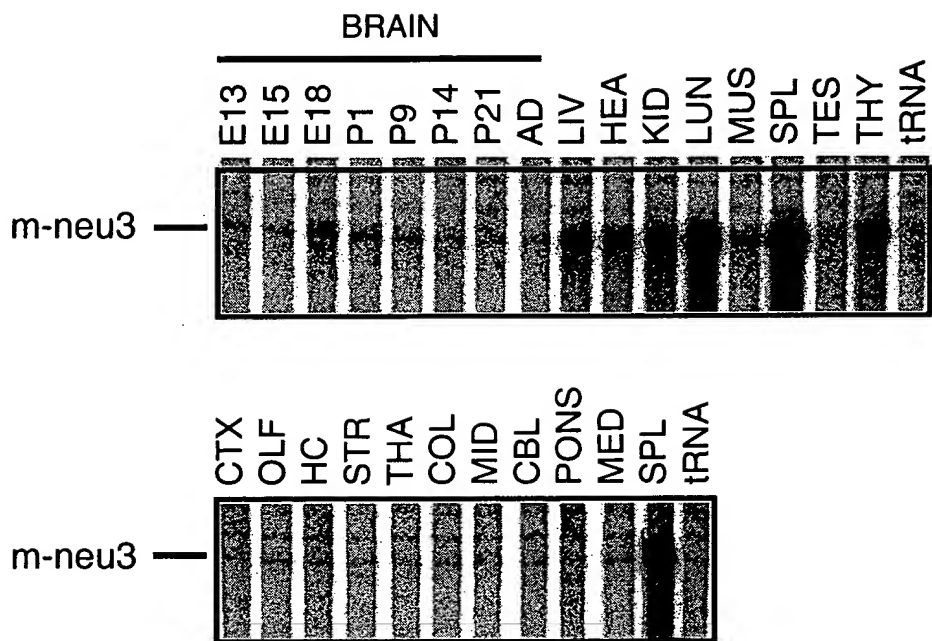


FIGURE 14

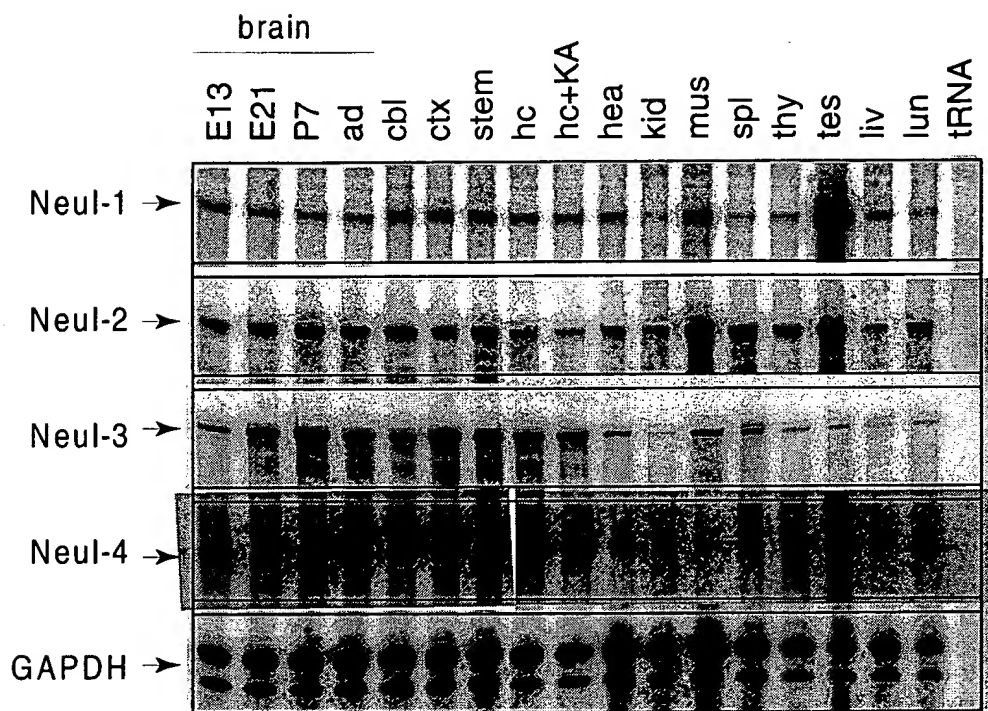


FIGURE 15